5-00449.

Sequence:

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Searched:

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X58242 C.ruminanti
AJ25271 Rickettsi
X9276 F.falciparu
AF07261 Reclinomo
AL139076 Campyloba
U3741 Drosophila
U11584 Drosophila
AC005504 Plasmodiu
AC001398 Plasmodiu
AL034556 Plasmodiu
AL034556 Plasmodiu
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RC005504
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2.7 69034
2.7 317511
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Submitted (11-NOV-1998) S.G.E. Andersson,
Siv. Andersson@molbio.uu.se, Dept. of Molecular Biology, University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete genome; segment
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiacea: Rickettsiaes; Rickettsia; typhus group.
1 (bases i to 312430)
Andersson, S.G., Zomorodipour, A., Andersson, J.O.,
Sicheritz-Ponten, T., Alsmark, U.C., Podowski, R.M., Naslund, A.K.,
Eriksson, A.S., Winkler, H.H. and Kurland, C.G.
The genome sequence of Rickettsia prowazekii and the origin of
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Pred. No. 2.4e-28;
0; Mismatches 89;
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Nature 396 (6707), 133-140 (1998)
   /transl_table=11
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complete genome.
Rickettsia prowazekii.
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Andersson, S.G.E.
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AL031746 Plasmodiu
U79210 Human clone
AF044321 Homo sapi
U49822 Saccharomyc
AL033475 Plasmodiu
298745 Human DNA s
AC008132 Homo sapi
AC005678 Homo sapi
AC0133123 Caenorhabdi
AE003846 Drosophil
AE003846 Drosophil
AC01429 Plasmodiu
AC01429 Plasmodiu
AC07324 Homo sapi
AL031746 Plasmodiu
U11584 Drosophila
U37541 Drosophila
AC008206 Drosophil
AC005504 Plasmodiu
AC004157 Plasmodiu
AC004157 P. Falciparu
AC004948 Homo sapi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sap
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Waghela,S.D., Rurangirwa,F.R., Mahan,S.M., Yunker,C.E.,
Crawford,T.B., Barbet,A.F., Burridge,M.J. and McGuire,T.C.
A cloned DNA probe identifies Cowdria ruminantium in Amblyomma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Cowdria.
1 (bases 1 to 1306)
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/strain="Crystal Springs (Zimbabwe)"
/db_xref="taxon:779" (Zimbabwe)"
/clone="lip="genomic: E.coli puC 19"
/clone="pcS20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microbiol. 29 (11), 2571-2577 (1991)
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heartwater rickettsia.
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SPAC1420
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Submitted (08-MAR-1991) T.C. M
Dept. of Vet-Micro/Pathology,
                                                                                                                                                         AC007708
                                                                                                                                                                           PFMAL1P3
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CRPCS20
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ARGNATURUKNAMRAKGYN"
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EDILETASIVLSIFIVEPSFGGGTKEKLVSNGVSKLVENIIKDHFDHFLSSDKVLATH
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IEWECEVEVPSDIPKKALINFPNGLKDYLSSKISLDNLVIPEIFSGNIESTVDDIKLE
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        Uppsala, Husargatan 3, Uppsala, S-751 24, SWEDEN
Nov 13, 1998 this sequence version replaced gi:3860788.
Location/Qualifiers
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                                                              FEATURES
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                                      COMMENT
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X952/6.1 GI:1171591
Clp gene; LSU TRNA gene; ORF105; ORF129; ORF78; ORF79; ORF91; rpl14
clp gene; LSU TRNA gene; rpl23 gene; rpl36 gene; rpl36 gene; rpl3 gene; rpl3 gene; rpl3 gene; rpl3 gene; rpl3 gene; rpl3 gene; rps1 gene; rps3 gene; rps1 gene; rps1 gene; rps1 gene; rps1 gene; rps3 gene; rps1 gene; rps1 gene; rps1 gene; rps3 gene; tRNA-Asp; tRNA-Cli; tRNA-Gli; tRNA-Gli; tRNA-Gli; tRNA-Try; tRNA-Try; tLNA-Try; tLN
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J. Mol. Biol. 261 (2), 155-172 (1996)
96346169
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P.falciparum complete gene map of plastid-like DNA (IR-B).
X95276
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                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
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REFERENCE
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                                                                                                                                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91604 AATAAGGATATAATAGGTACATCGATATATATGTTACTCCAAATAAAGCAGGGAAATAT 91663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91424 ACTACTATTAAAGAAACAGTTAGTGTATATTCTAAGGTAAAAGGTACTAAAAGCTATAATT 91483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 acagtaag-----aacaagtaatatatcaaattctaaaataggtaacactattattaaa 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     429 ataatgccagtatcattttttatagatccagccatagaaacagatcctgaaactgctgac 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity 55.7%; Pred. No. 2.1e-10; Similarity 55.7%; Pred. No. 2.1e-10; Conservative 0; Mismatches 248; Indels 6;
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/protein_id="CAA14698.1"
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                                                                                                                                                                                                                                                                                                                                                     /gene="trNA Met (CAT)"
11279 11352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(12284. .12769)
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Pred. No. 2.5e-09;
0; Mismatches 1938; Indels
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Best Local Similarity 44.1
Matches 1583; Conservative
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1554 AGGTAAATTTAAAATTTTTAAGTTTATTGGGGTATTATATTTTAGAT 1484 acatgaaattagcaactacaaagaagttgctgaagccttcataagctacattatag 1484
4 4 0 4 0

2139 2486 tcacagatcaagaaatattcaatagaataatagcagaacagattgcacatgttaaatcat 2723 ggtagaaccaccgcataaaacaaatatgactttaacattaaaagacagttcagtagaaat 1723 gtaatatttacgataccatagacaaagtaagtatccaagatgttaactccgctatggaaa 2199 AAAAATAAGTTATTATTTGAAATAAGTAAAATTTCAAATAATATTATTATTATACTATAACA 4848 cccagaactgittitaaigiatcaaataccaaatggiattaccaataaaaactacataci 1783 taacatgatgttagcagaaatactcggtagtggtaaattcagcct.gctttacaatgatt 5029 TATAAAAATATATGATAATAGAAATGAAATTATTATAAATGAT-TATATATTAAAT attataaaaaagtaaatattgtaataataaagtaataaaaattatatgatatatataaa ctttcatatcatatttttatggcatgcatctaatactaggagtaccgctatcagaaatca atatettteaaaacaatataagattaacegggeatttattaeetaatggagaatagttat 2313 atgcaaatgatctcaatattaacataaaagaagctacaactaaaaataaaatacactatc tatatgttg-----aacatcataacctaccaacaatttccttaaaaatttgcattcaaga aagcaggatacgcttatgatgcctttgataagcaaggacttgcatactttacatcaaaaa tattaaacgaaggatcaaaaaacaactatgctctcagttttgcacaacaattagaaggca aaggtatagacttaaaatttgatatagacctagacaatttttat---atatcattaaaaa cettateagaaaactttgaagaageeetagttttaeteagtgattgeatatteaacaeeg tggtaattaacaatccaatagttacatcgataaaaaacagattataattacttaactgaca tagaaagtgcaaagtataaagtaaaa---gcacatttaacttatgcatttgacggactaa 5148 TAGTATATTAGATGTAATAGATAATAGTGGTATATTTAAATTTTAAATATATTTGTACTTT aacaagaaattcataaatgtataaataattatttagaaaatggaatttcagcagaatatt gogataattacctttccattgaagctatacctaaaaacgggatctctacagaagctgtag 5268 TAATAATAATTATATAAAAATCAGATAAATGTAAAGGTATTTTAGTACAACAAAAAA 1843 2140 2200 2373 5508 5627 2664 4729 4849 1903 1963 5088 2023 2080 2487 2547 2604 1664 1724 1784 2427 5687 D_D qq g d δ Dp δ g Qy Db õ g QY Db Q D οy a οy q Οy g οy g δ g δ g δy g ò δ δ ò Q

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DEFINITION
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VERSION
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TITLE
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Chases 1 to 69034)
Lang, B.F. and Burger, G.
Direct Submission
Submitted (06-JUN-1997) Departement de Biochimie, Universite de
Montreal, 2900 Edouard-Montpetit, Montreal, Quebec H3T 1J4, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lang, B.F., Burger, G., O'Kelly, C.J., Cedergren, R., Golding, G.B., Lemieux, C., Sankoff, D., Turmel, M. and Gray, M.W. An ancestral mitochondrial DNA resembling a eubacterial genome in
                                                                                                                                                                                                                                                                                                                                                                     03-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrion Reclinomonas americana
Eukaryota; Reclinomonas.
1 (bases 52095 to 54121)
Burger,G., Lang,B.F., Reith,M. and Gray,M.W.
Genes encoding the same three subunits of respiratory complex
are present in the mitochondrial DNA of two phylogenetically
distant eukaryotes
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Lang, B.F., Goff, L.J. and Gray, M.W.
A 5 S rRNA gene is present in the mitochondrial genome of the Protist Reclinomonas americana but is absent from red algal
                            atcaaattttctttacaggattatattgtgacctaccataacaacttatatttagaaaat
                                                                                              gacaacagatacacatcaataaattatcactacaattcaattaataaaacaatgagta
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Reclinomonas americana mitochondrial DNA, complete genome
                                                                                                                                                                                            3921 tttttacttaattatttaattttattttttaaaataaaaattacaatttact 3972
                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 93 (6), 2328-2332 (1996)
96197311
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/gene="trnL(gag)"
complement(3054, .3127)
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AUTHORS
TITLE
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SILNIYVNNKFISNDKFLNHDLFLLDIYKDNKSIFIIENTNDDFSPPLELLNKVGSHL
SEKNBDFLFELIENKNINYQYIFINLKEQPDGITBSEKKKLLLMFPKSKHVL
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6570. .11006
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KIRGLKGRSIOLYFTDNIGQKLDTRTLISGKNLMQNITHQEIDKLLDSFKISFKE
IGETFTYSITEYKYCNMGWFIDFNWKEISKYFFIKKNKNIISTSLSFDNNLLANNDYI
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RYGNKGVISRILSLEDMPYLRDGTPLDIVLSPLGVSSRMNIGQLLECHLGLAGVELSK
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FLQNFIRGKTSRIDIPRTFKLLRDELRVLGMELNFIVKRSNE"
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LKMRDLNICSGTSLKNLKTYDDFKQILFNKFTINLVFKLINSIISKHPVLLENFRFIL
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PISFKLDKDNVVLTTSGRILLYYLLLEFVNIDFKYVNKVFDKKEIVSLIKMISNLNNL
NKTSFILDQIMSFGFYYAYKAGISLHKNDINTPNLKELFVYKTKKKVEDDLKNFSRGI
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NKLIVYDKSIRYKNKKKGVVIQIAKFFDSLVDLNKHYITTSNLOKSTESLLSYIYKEE
KIRLMFLSYLFFIFKNKYKYDLGIKKKIILDDLNIHLNQKMNMSFSSFYTKTILYRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISIDEKSKRLLNEWSKCSSILANQILKDVIYTVPNRKSSIYMLINSGARGSMVOMRQL
CGIRGLMIRESGDILEIPIISNEKEGLSVODYRNSHGARKGYUDTSLKTAASGYLTR
KLFYAAKDLFITELDCGTRKGIIFGNLKYORDGYKIDSFYKNIVGRILVRNIKNFYTG
EILVKKGLIYTNLVLMLIKFGIEFVVTRSPMTCETRNGICRKCYGSIGNNNEIVSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNIKLNFDLIYKMYLLICYKYLFSIEIFLKKNKKDLLKECIKODNFKYVDIRFKNMYR
EIYKRNKKNDFVLLNIKMSLSKVFFIDLKKKIPYSMEFLLKNFILQEMYILLFLYYIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RMNIQTFSPLLIYTKAIQLHPLVCSSFNADFDGDTMAIYIPHTLRSQIESRVLMMSST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="RNA polymerase subunit beta'"
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11093. 15247
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/gene="rpoB"
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                                                                                                                                                                                                                                                                                                                                       6570. .11006
/gene="rpob"
6570. .11006
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57.78;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                             gene
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                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MTIINKTAQTLELTELVKGMSLTLDYFFRKKYTLNYPFEKGPLS
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IYCGFCQEACPVDAIVEGPNFEFATETHEELLYDKEKLLQNGDRWETEIAANLANEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MNKIIGFIRLEIESGKASPSPPVGPALGLRGVNIMOFCKEFNNR
CKQLNIKDGVPVPTIITVYDDKTFSFKMKTPSITYFIKKHLEISKGASKPGKENFLNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tianslation="MSLQEFHNVEDAVKLLKCYNLNDKNLDSKIIVGFVFNKTKSISK
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/note="signal element domV"
/note="Region: Signal element domV"
4663. 4697
                                                       .3093, aa:Pro)
                                                                                                                                                                                                                                                        .3180, aa:Lys)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /anticodon=(pos:4131. .4133,aa:Trp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product-"ribosomal protein L11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="codon recognized: UGG"
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                                                                                                                                                                                                 /note="codon recognized: AAA"
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/note="signal element pal2"
complement(3252. 3740)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAD11861.1"
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/note="^-"
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/gene="trnK(uuu)"
                                                    /anticodon=(pos:3091. .3
complement(3054. .3127)
/gene="trnP(ugg)"
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4136. .4662
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4742. 5179
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5207. 5881
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                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="nad8"
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/product="putative ATP /GTP-binding protein"
/product="putative ATP /GTP-binding protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                             jēi..768

gene—"Cj0668"

/note—"Cj0668, probable ATP/GTP-binding protein, len: 135

aa; similar to hypothetical proteins e.g. YJEE_ECOLI (153

aa), fasta scores; opt: 164 z-score: 205.3 E(): 0.00039,

33.8% identity in 80 aa overlapp. 44.2% identity to HP0716.

Contains PS00017 ATP/GTP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Cj0669"
/gene="Cj0669"
/gene="Cj0669"
/force:"Cj0669, probable ABC-transporter ATP-binding
protein, len: 242 aa; highly similar to many e.g.
YHBG_ECOLI probable ABC transporter ATP-binding protein
(240 aa), fasta scores; opt: 840 z-score: 1144.2 E(): 0,
54.28 identity in 236 aa overlap. 65.8% identity to
HP0715. Contains PS00017 ATP /GTP-binding site motif A
(P-loop) and Pfam match to entry PF00005 ABC_tran, ABC
transporters"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="PS00017 ATP/GTP-binding site motif A (P-loop)" 761. .1489
                                                                                                                                                    hypothetical proteins e.g. YABO_BACSU (86 aa), fasta
scores; opt: 149 z-score: 259.2 E(): 3.8e-07, 35.4%
identity in 79 aa overlap. 43.6% identity to HP1423"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Pfam match to entry Pr00005 ABC_tran, ABC
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                                                                                                                                  similar
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119. .364
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761. .1489
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361. .768
                                                                                     119. 364
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                                                           /gene="Cj0667"
119. .364
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The genome sequence of the food-borne pathogen Campylobacter jejuni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19745 AACATTAAAAGATGAACAACAAGAGAATAGGATAATAACTGTACGTTTTAATGGTGATGT 19804
                                                                                                                                                                                                                                                                                                                                                             19864
                                                                                                                                                                                                                                                                                                                                                                                                                                    20045 TATAGATCCTGCAATTTTAGATGATCCTAAAATGTCTGATATTGATTCAATAACTTTATC 20104
                                                                                                                                                                                                                                                                                                                 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CJ11168X3 317511 bp DNA BCT 08-JUL-200
Campylobacter jejuni NCTC11168 complete genome; segment 3/6
AL139076 AL111168
                                                                                                                                                                                                                                                                                                                                           19685 TIGICAAGIAACIGGIIITIGGCGGAACAACACAAGIIGCIGAIITAGAAICAGAIATITI
                                                                                                                                                                                                                                                                                                                                                                                                             agaacaaaaattgattttctaccgcgcagaaaatctacttgatgaggacacttcaggaat
                                                                                                                                                                                                                           ------aaataggtaacactattaataaagtcagatttaatgcagatat
                                                                                                                                                                                                                                                                                                                   acacaaacaactgccatggaaattctatccagaagtatctcatgtatttgtaaaaccagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tatagatccagccatagaaacagatcctgaaactgctgacgtaaaactcatcactcttc
21;
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Location/Qualifiers
0; Mismatches 192; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Campylobacter jejuni"
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL139076.2 GI:6968128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 317511)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Details of C. jejunis
on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Conservative
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291;
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ACCESSION
VERSION
KEYWORDS
SOURCE
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  Matches
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AUTHORS
TITLE
JOURNAL
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LOCUS
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REFERENCE AUTHORS JOURNAL MEDLINE

TITLE

FEATURES

COMMENT

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Similarity
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Matches
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                                                                                                                                                                                                                                                                                                                               /product-"RNA polymerase sigma-54 factor"
/product_ald="CAB72947.1"
/db_xref="G1:668132"
/translation="MLKQKITQAPKTKISOTLRSWLPILQANIEDLKENLDKFAEDNP
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SQELAKKIIECLNEGSYFEHDEEFLKEYSLEBIERVRARFKFLDPVGVQARAYKSAFL
FALENMELDEDIDEFCRMLIMDFENIONYTKEPLYKEALAVLKRFSTPPFLEYFEDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIVPDIFVYKENGEIKVKINDDYYPEISIQTOGLEHDFLSHYIKEAKNIVDALAMRKA
TLYKIGLMYVEXQYDFMGKEIKPMFKDLALDLERRASTISRAVAKKLSCERGLIP
LRDFRFALDEEGETSNYGKEFVANLVKNEDRNKPLSDSKILELIKEEFKVDIGRRT
ITKRRKHLANASSTORKKLYELEG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 //note-"cj0671, dcuB, probable anaerobic C4-dicarboxylate
transporter, len: 474 aa; highly similar to e.g.
COUE_ECOLI anaerobic C4-dicarboxylate transporter (446
aa)opt: 1280 z-score: 2918.6 E(): 0, 69.1% identity in 466
aa overlap. No Hp ortholog. Also similar to Cj0088, dcuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
/product="putative anaerobic C4-dicarboxylate transporter"
/product="putative anaerobic C4-dicarboxylate transporter"
/db_xref="c1:608133"
/translation="MPELTSLSEAGOFAIQIIIVLICLFYGAKKGGIALGLLGGIGIL
MLVFAFHIKPGKPAIDWALTILAVVVASATLQASGGLDVMLQIAERILRRNRKFLTL
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AVVSLTALLINANHKAGFDGYINLLQTIPSTLFGVLCIGIFSWFGKDLDRDVBVFG
EKLKDPEFKXYYGDSKTLLGVKLPKSNWVAMMIFLGAIALVALLGVFDFLRNWGOV
VKNGTPQVDALGNPRMDVLSNVSVIOMFMLLAGSLIIIFTKTDAKKIGSNEIFKSGMI
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/note="C10676, kdpA, probable potassium-transporting
/note="C10676, kdpA, probable potassium-transporting
Afpase A chain pseudogene, len: 1744 bp; highly similar to
e.g. ATA-ECOLI potassium-transporting ATPase A chain (EC
3.6.1.36) (557 aa). No hp match. Note thay kdpB (C10677)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALVAVFGISWMADTWFAVHTPMMKAALGDIVKEHPWTYAVMLLLISKFVNSQAAAISA
FVPLALGIGVEPGVIVAFAAACYGYYILPTYPSDLATIQFDRSGTTHIGKFVINHSFI
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/note="Cj0670, rpoN, probable RNA polymerase sigma-54 factor, len 416 aa. similar to many e.g. RP54_BACSU RNA polymerase sigma-54 factor (436 aa), fasta scores; opt: 357 z-score: 603.0 E(): 2.7e-26, 28.9% identity in 443 aa overlap, and RP54_ECOLI (477 aa), fasta scores; opt: 365 z-score: 483.2 E(): 1.3e-19, 28.8% identity in 459 aa overlap. 47.4% identity to HP0714. Contains PS00718 Sigma-54 factors family signature 2, Pfam match to entry PP00309 Sigma-64 factors, and helix-turn-helix motif at aa 303-324 (Score 1227; +3.37 SD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Cj0672, possible periplasmic protein, len: 62 aa; no Hp match. Contains possible N-terminal signal sequence and second hydrophobic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="PS00718 Sigma-54 factors family signature 2" 2903. .4327 //gene="doub" 2903. .4327 2903. .4327
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/transl_table=11
/product="putative periplasmic protein"
/protein_id="cAB72949.1"
/db_xref="G1:6968134"
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/gene="Cj0672"
4469. .4657
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/gene="Cj0672"
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/gene="kdpA"
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/gene="rpoN
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/note="C10677, kdpB, probable potassium-transporting Arpase B chain, len: 681 aa; similar to e.g. ATKB_ECOLI potassium-transporting Arpase B chain (EC 3.6.1.36) (682 aa), fasta scores; opt: 2419 z-score: 2798.9 E(): 0, 56.6% identity in 678 aa overlap. No Hp match. Contains PS00154 E1-E2 Arpases phosphorylation site and Pfam match to entry PF00122 E1-E2_Arpase. Note that kdpA (cj0676) and kdpC //codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 134900 TTTTTTATAAAGTGGGTTCAAGAAATGAGATCATGGGAAAAAGTGGCATAGCTCATATGT 134959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 135020 TTAAGGGTTTTGGTGGTGTGGATAATGCAAGCACAGGTTTTGACTATACTCATTATATA 135079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135320 GTATTGAAGATATTAAAGAATTTCACAGTATTATTATCAACCTAAAAAATGCGATTTTAC 135379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 135440 AGATTAAAAATACTAAGACTATACCTAAAATTCACACAAAAGAGCCTAAGCAAGATGGAG 135499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1153 ttgaacacttaatgtttagtggaacagaaaatt-----tcctaatctcatcagcacac 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1327 attttaaggttaccgacaaagcattaataagagaacaaaaggtagtcttagaagaagaa 1386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1093 tattatacaaagtcggtggaactgatgatccagtaggatactctggattagcacatttt 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1504 acaaagaagttgctgaagcctttcataagctacattatagtcctaataatgctatattaa 1563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                   /transl_table=11
/product="pseudogene (potassium-transporting ATPase
chain)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaatgag---agttgaaagccaagcaaaaaaaacatactagaagaagaaatggaaaatgcat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1564 ttgtaactggagatgcagatccacaagaagtaatcacacttgcaaaacaatactatggga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 317511;
intact, while kdpc (Cj0678) is a pseudogene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.7%; Score 140.6; DB 2;
49.0%; Pred. No. 1e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /EC_number="3.6.1.36"
                                     /codon_start=1
                                                                                                                                                                                                         5521. .5529
/note="G(9)"
6371. .8416
/gene="kdpB"
6371. .8416
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/gene="kdpB"
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LSDNNNLMSTEASLKYFLTOVLASTVLLFSSILLMLKNNMNNEINESFTSMIIMSALL
LKSGAAPFFFFWFPNMMEGLTWMNALMLMTWOKIAPLMLISYLNIKYLLLISYLLSVILSVI
SAIGGLNOTSLRKLMAFSSINLGMMLSSLMISESIMLILFFYSFLSFVLTFWFNIF
KLFHLNOLFSWFVNSKILKFTLFMRELSLGGLPPFLGFPFKRIVJOQUTLCNOYFMLT
IMMMSTLITLFFYLRICYSAFMMNYFENNWIMKMNMNSINYNMYMINTFSIFGLFLI
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/db_xref="G1:1166530"
/translation="MFNNSSKILFITIMIIGTLITVTSNSWLGAWMGLEINLLSFIPL
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first codon uncertain"
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                                                                                                                                                                              Ballard,J.W., Olsen,G.J., Faith,D.P., Odgers,W.A., Rowell,D.M. and Atkinson,P.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 (bases 1 to 19517)
Lewis, D.L., Farr, C.L. and Kaguni, L.S.
Direct Submission
Submitted (03-007-1995) Laurie S. Kaguni, Biochemistry Department, Michigan State University, East Lansing, MI 48824-1319, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /noTe-"derived from new and previously submitted sequences; sequence is a composite containing sequences obtained from different Drosophila melanogaster strains"
                                                                                                                                                                                                                         Evidence from 12S ribosomal RNA sequences that onychophorans are
                                      Satta, Y. and Takahata, N. Evolution of Drosophila mitochondrial DNA and the history of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    completion of the
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Lewis,D.L., Farr,C.L., Farquhar,A.L. and Kaguni,L.S.
Sequence, organization, and evolution of the A+T region
Drosophila melanogaster mitochondrial DNA
Mol. Biol. Evol. 11 (3), 523-538 (1994)
                                                                                                             87 (24), 9558-9562 (1990
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/protein_id="ARC47812.2"
/db_xref="GI:7412849"
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Lewis,D.L., Farr,C.L. and Kaguni,L.S.
Drosophila melanogaster mitochondrial DNA: comple
nucleotide sequence and evolutionary comparisons
Insect Mol. Biol. 4 (4), 263-278 (1995)
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/product="NADH dehydrogenase subunit 2"
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/organelle="mitochondrion"
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/note="derived from new and ;
sequences; sequence is a com;
                                                                                                                                                                                                                                     modified arthropods
Science 258 (5086), 1345-1348 (1992)
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/product="tRNA-Tyr"
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/product="tRNA-Cys"
                                                                                 melanogaster subgroup
Proc. Natl. Acad. Sci. U.S.A.
91088557
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/product="tRNA-Gln"
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/product="tRNA-1le"
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Transfer RNA genes in Drosophila mitochondrial DNA: related 5'
flanking sequences and comparisons to mammalian mitochondrial tRNA
135554 ATAAAATTCCAAATTTCA--AGCACAAAGATATACCTGCTTTAAATGCT-TTATCCGAGC 135610
                                                                                                                                                                                                                                                            Db 135728 TITGTAATIGTAACCCCCAATGTTAATGCAGAAAAGTAGAAAAAGTAGAAAAAGTITTAAAAATCA 135787
                                                                                                                                                                                                                                                                                                                                                          TIGATAAACTTAAAATGGGTAAAATTTCTCAAAAAGATTTGCAAAAGAGGTGAAAAATAATG 135847
                                                                                        D 135848 TCAAAAGTGATTTTATTTTCTCACTTAACAATGCTAGTGCAGTGGCAATATTTATGGTT 135907
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Satta,Y., Ishiwa,H. and Chigusa,S.I.
Analysis of nucleotide substitutions of mitochondrial DNAs
Drosophila melanogaster and its sibling species
Mol. Biol. Evol. 4 (6), 638-650 (1987)
                                                                                                                                                                                                                                                                                                                          taaataattatttagaaaatggaatttcagcagaatatttagaaagtgcaaagtataaag
                                               tactoggtagtggtaaattcagcctgctttacaatgatttggtaattaacaatccaatag
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Nucleic Acids Res. 10 (21), 6619-6637 (1982)
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Mitochondrion Drosophila melanogaster
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Nature 304 (5923), 234-241 (1983)
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de Bruijn, M.H.
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14949 ATATTAATAATTTTTATAAAAATAATTTTTTAAAGAAAAATTAAAATTAAATTTAATTAA 15008
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/transl_except=(pos:complement(6401. .6402),aa:TERM)
                                                                                                                                                                                                                                                                                                                                                                                                              490 taaaaactcatcactctttcatatgtattctttaagtacaaagaataaacttcatataccg
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                                                                                                                                                                                    complement(6401. .8124)
/note="TAA stop codon is completed residue to the mRNA"
                                                                                                                                                                                                                                                                                                                                              Pred. No. 4.3e-08;
0; Mismatches 1988;
                                                                                                                                                                                                                                                                                                                          Score 138.2;
                                                                                                                                          complement(6337. .6401)
/product="tRNA-Phe"
                    /product="tRNA-Asn"
6184. 6251
                                                                                                                            /product="tRNA-Glu"
/product="tRNA-Arg"
                                                                                    /product="tRNA-Ser"
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                      LLPPALSLLLVSSMVENGAGTGWTVYPPLSAGIAHGGASVDLAIFSLHLAGISSILGA
VNFITTVINMRSTGISLDRMPLFVWSVVITALLLLLSLPVLAGAITMLLTDRNLNTSF
FDPAGGGDPILYQHLFWFFGHPEVYILILPGFGMISHIISQESGKKETFGSLGMIYAM
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SPÄLWALGFYCELTYGGLTGVVLANSSVDILLHDTYXVVAHFHYLLSKOAYFALMAGF
IHWYPLFTGLTLNWRLKSHFIIMFIGVNLTFFPQHFLGLAGAPRYSDYDDAYTTWN
IVSTIGSTISLLGILFFFFIIWESLVSQRQVIYPIQLNSSIEWYQNTPPAEHSYSELP
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MANSILLIHERKTILGSGHNGSPFIFISLESLILENNHWGLEPYIFFTSHTTLTL
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LTANNIAGHLLLTLGNTGSSMSYMLMTFLLMAQIALLVLESAVAMIQSYVFAVLSTL
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PKSSSRLPFSLRFFLITIIFLIFDVEIALILPMIIIMKYSNIMIWTITSIIFILILLI
GLYHEWNQGMLNWSN"
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LFFNNYVNRFLLHGQLIEMIWTILPAIILLFIALPSLRLLYLLDEINEPSVTLKSIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QWYWSYEYSDFNNIEFDSYMIPTNELMTDGFRLLDVDNRVVLPMNSQIRILVTAADVI
HSWIVPALGVKVDGIPGRLNQINFFINRPGLFYGQCSEICGANHSFMPIVIESVPVNY
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FYESLSPAIELGASWPPWGIISFNPFOOLPLLWARTLLASGVTWWAHHSLWENNHSOT
TQGLFFTVLLGIYFILQAYEYIEAPFIIADSIYGSTFFWATGFHGIHVLIGTTFLLV
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  ALIGDDQIYNVIVTAHAFIMIFFMVMPIMIGGFGNWLVPLMLGAPDMAFPRMNNMSFW
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/note="TAA stop codon is completed by the addition of
residues to the mRNA"
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/transl_table=5
/product="cytochrome c oxidase subunit III"
/protein_id="AAQ47816.1"
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3083. .3767
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5608. .5961
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6055. .6118
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16020 ATAAAAAATGAAAATTAATTCCCCCTATTCATAAATTTATTGTATAATTAAAACT 16079 acaatggatatggcagaccagtagtaggatgggaacatgaaattagcaactacaacaaag 1509 16500 ATAAATAAAATTATTTAAAATAATTAATAAGAAATAT----TTTTATTATAATAAAAT 16554 16615 AATTTTCAATTAAATTATATAAATATAAAAAATATAATTTTTAATTATTTAATCACTAAATCTGAA 16674 1570 ctggagatgcagatccacaagaagtaatcacacttgcaaaacaatactatgggaaaatac 1629 tgactttaacattaaaagacagttcagtagaaatcccagaactgtttttaatgtatcaaa 1749 1810 gtagtggtaaattcagcctgctttacaatgatttggtaattaacaatccaatagttacat 1869 2103 atgcatctaatactaggagtaccgctatcagaaatcagtaatatttacgataccatagac 2162 1510 aagttgctgaagcctttcataagctacattatagtcctaataatgctatattaattgtaa 1569 1924 aagctatacctaaaaacgggatctctacagaagctgtagaacaagaaattcataaatgta 1983 1390 tgagagttgaaagccaagcaaaaaaaacatactagaagaagaaatggaaaatgcattttatt 15902 ATTTATATATATATATATATATA--TAATTTTAATTTTCAATTAAATTATAAATATAA 1984 taaataattatttagaaaatggaatttcagcagaatatttagaaagtgcaaagtataaaag catctaataataagaaaccttcaagtcaagttagggtagaaccaccgcataaaacaaata taccaaatggtattaccaataaaaactacatacttaacatgatgttagcagaaatactcg cgataaaaacagattataattacttaactgacagcgataatt-----acctttccattg aaagtaagtatecaagatgttaaeteegetatggaaaatatettteaaaacaatataaga ttaaccgggcatttattacctaatggagaatagttatgagaaacatattgtgttacacat ----gatctcaatat taatattgattttcttttcattcaatacatatgcaaat· 1450 2332 2163 셤 셤 요 8 g g ð g ò g Q g ç g ò g ò g õ g ò g g 셤 g 셤 à ò ò δ ö ò ò ò ö

17515 ITTAAATAATTTAATATAAATTTTTTAAAAATTTCTTAAATGTATTATTATTTTTATAAAAA 17574 ATTCAATTCATATTTATATATATATACATATAATTTAATTTTCAATTAAATTATATA 16974 16675 ATAATTAATTATATATATATATATATATAAAAAAATGAAAATAAATTAATTCCCCCTA 16734 17035 ATATATATATATATGTAAATGAAATAAATTTATTCCCCCTATTCATAAATTTATAT 17094 aataccataccagatacgactgitaatagagaagacacattattatatgtacagagat 3040 gtaccacaaagtgtcataatgtttgctacagacacagtaccatatcacagcaaagactat 3100 tatatccgtcttaacagatattatagagcacattaaaaagtatggagttgatgaagacac 3339 taatgttagtgagatattgttaagcttacaattacacgatctagatccgagttatattaa 3459 ctacaacagaaatgaatcacgctatattcaaagggcacccatattctaacaaagtttacg 2807 aatca-tagtaatgtgctatttggtacaatattcactgataataccacagtaacaaaatg aaaaatagttttgacaaggaacaaatcgttatcagcgcagcaggagatgtagatccaaca catgcatcaaacttgttcaatactatgctaggcggattaagtctcaattcaatattaatg atagaattaagagacaagttaggattaacataccatagtagcagttcactatctaacatg cctaccaacaatttccttaaaatttgcattcaagaaagcaggatacgcttatgatgcctt atatagacctagacaatttttatatatcattaaaaaccttatcagaaaactttgaagaag ccctagttttactcagtgattgcatattcaacaccgtcacagatcaagaaatattcaata gaataatagcagaacagattgcacatgttaaatcattatattctgctcctgaatttatag ggacattaaatacaatcaataatatcaaccaggaagacgttgc-----attatatata ttttgcaattgcaaaatctagtattaccaactcttttattttatctatgttaaataacaa ctatgctctcagttttgcacaacaattagaaggcaaaggtat----agacttaaaatttg cagctatcaaatttactagataaatatattctttccaaattgccatctggtaataacaaa 2392 2452 2688 2748 2808 3041 3101 3340 16735 2568 2861 2981 17575 16975 17155 3161 17455 3221 3280 17635 3400 g qq g 8 g g 셤 g g g QQ g g g g g g ö ö ò ò ò ò ò οy ö 원 ò õ οy à ò ò ò

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Lewis, D.L., Farr, C.L., Farquhar, A.L. and Kaguni, L.S. Sequence, Organization and Evolution of the A+T Region of Drosophila melanogaster Mitochondrial DNA
MOI. Biol. Evol. 11, 523-538 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUL-1994
                                                                                                                                                   3580 acaaatagatgcta-aaaaacacataccttggttaagtatacaggttattgtatttacta
                                                          3520 aattttatctaatgaattagtaataattgaagtaggaaaaaacaataacataaatggcaa
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Drosophila melanogaster Oregon-R mitochondrial A+T region.
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Submitted (28-JUN-1994) Laurie S. Kaguni Ph.D, Dept. of
Biochemistry, Michigan State University, East Lansing, MI,
48824-1318, USA
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Mitochondrion Drosophila melanogaster
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422 aaaaactataatgccagtatcattttttatagatccagccatagaaacagatcctgaaac 481
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ilarity 43.2%; Pred. No. 7.6e-08;
Conservative 0; Mismatches 2024; Indels 60;
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/note="deoxythymidylate stretch"
131 c 74 g 2125 t
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/note="deoxythymidylate
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/note="repeat II-A"
/rpt_type=tandem
3113. 3576
                                                                                      1361. [1705
/note="repeat I-C/A"
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/note="repeat I-C"
                                                                                                                    /rpt_type=tandem
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2649. .3112
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complement(4565.
/note="repeat I-/
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1361. .1705
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4041. Aso.
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oy og	TITIAAAAAAAAAAATGATTATTAAATTATACTTAATAAACTATTITATAATAAATTATT 123
Oy	960 tttttcatagttttcttaacaatagccaatcatgctttatcctttaacattaaagttaca 1019
Dp	
Oy	1020 catgaaaattagataatggaatggaagtatacgtgattccaaatcatcgcgcaccagca 1079
Db	
Oy	1080 gtcatgcacatggtattatacaaagtcggtggaactgatgatccagtaggatactctgga 1139
Dp	
Oy Ob	1140 ttagcacatttttttgaacatttaatgtttagtggaacagaaaatttcctaatctcatc 1199
9	1200 agcacacttagtaatataggcggaaatttcaatgcaagcacatctcaattttgtactata 1259
9	
9 9	1260 tactacgaattaataccaaaacaatatttatctttgcaatggatattgaatcaga 1315
9	1316cagaatgcagaattttaaggttaccgacaaagcattaataagagaacaa 1364
9	
S S	1365 aaggtagtottagaagaaagaaaatgagagttgaaagccaagcaaaaaacatactagaa 1424
9.	1425 gaagaaatggaaaatgcatttattaccaatggatatggcagaccagtagtaggatgggaa 1484
2.	
o S S	1485 catgaaattagcaactacaacaaagaagttgctgaagcctttcataagctacattatagt 1544
oy	1545 cctaataatgctatattgtaactggagatgcagatccacaagaagtaatcacactt 1604
Dp	
oy	1605 gcaaaacaatactatgggaaaataccatctaataataagaaaccttcaagtcaagttagg 1664
Ob	
<u>ک</u> ۾	1665 gtagaaccaccgcataaaacaatatgactttaacattaaaagacagttcagtagaaatc 1724
g ç	1725 ccagaactgtttttaatgtatcaaatgccaaatggtattaccaataaaaactacatactt 1784
S G	1785 aacatgatgttagcagaaatactcggtagtgattcagctgctttacaatgatttg 1844
ري	1845 gtaattaacaatccaatagttacatcgataaaaacagattataattacttaactgacagc 1904
10 مع	
Oy	1905 gataattacctttccattgaagctatacctaaaacgggatctctacagaagctgtagaa 1964
Op	
ογ	1965 caagaaattcataaatgtataaataattatttagaaaatggaatttcagcagaatattta 2024

tgtacagagagatgtacca----caaagtgtcataatgtttgctacagacacagtacca 3082 AATATAAATTTTTTAAAAATTTCTTAAATGTATTATTTTTATAAAAAAATTTTTATATAAT 2670 2501 atataaaaaatagttttgacaaggaacaaatcgttatcagcgcagcaggagatgtagatc 2915 tggtaataacaaaaataccataccagatacgactgttaatagagagacacattattata 3027 atatcatatttttatggcatgcatctaatactaggagtaccgctatcagaaatcagtaat 2144 atttacgat-accatagacaaagtaagtatccaagatgttaactccgctatggaaaatat 2203 2911 TAATTTATAAAATTTATATTCCCCTATTTATTTATTAATTTAATTTATATA 2969 3030 TAATATATATATATATAGAAAATTAAATTATTTAAATTAATTAATATAAATTITTA 3089 caacacagctatcaaa-----tttactagataaatatttctttccaaattgccatc 2967 gaaagtgcaaagtataaagtaaaagcacatttaacttatgcatttgacggactaactttc 2084 aaatttgatatagacctagacaatttttatatatatcattaaaaacctta----tcagaaa ctttcaaaacaatataagattaaccgggcatttattacctaatggagaatagttatgaga aacatcataacctaccaacaatttccttaaaatttgcattcaagaaagcaggatacgctt atgatgcctttgataagcaaggacttgcatactttacatcaaaaatattaaacgaaggat caaaaaaacaactatgctctccagttttgcacaaca-attagaaggcaaaggtatagactta actttgaagaagccctagttttactcagtgattgcatattcaacaccgtcacagatcaag aaatattcaatagaataatagcagaacagattgcacatgttaaatcattatattctgctc ctgaatttatagctacaacagaaatgaatcacgctatattcaaagggcacccatattcta acaaagtttacgggacattaaatacaatcaataatatcaaccaggaagacgttgcattat AAAATTTCTTAAATGTATTATTTTTATAAAAATATTTATATAATAAAATCATGTTTTTT 2311 2371 2145 2431 2611 2671 2442 2502 2561 2616 2676 3090 3150 2916 3210 2025 2085 2204 2264 2551 2323 2382 2736 2796 2856 3028 음 g g ö 8 ò g ò g 9 g à Dp S S S οy g Q Db ά පු ò g ò g ò ò g οy g ò g ò 원 ò ò

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TITLE
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AUTHORS
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                                                                                       AATTATTATATATATATATATTATATTATTATTGAATATTTATATATATATATATATATAT
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                                                                                                                                                                               ATITITIAATAAATTITIAATAATGAAATATAAATTITATTITITICAATTITITIAAA
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                                                                                                                                                                                                                                                                                              gatccgagttatattaataaatacaattcttactacaaagcaataacaatagaagaagta
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E (bases 1 to 104992)

S Hyman R.W., Qin.P., Pung, E.L., Conway, A.B. and Davis, R.W.

Binan R.W., Qin.P., Pung, E.L., Conway, A.B. and Davis, R.W.

Direct Submission

Submitted (21-AuG-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto, CA

On Apr 2, 1999 this sequence version replaced gi:4337172.

* NOTE: This is a "working draft" sequence. It currently

* consists of 3 contigs. The true order of the pieces

* son on the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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                                                                                                                                                                                                                                                                            Tamaki, T., Kurdi, O.B., Conway, A.B.
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                         Plasmodium falciparum chromosome 12, *** SEQUENCING IN PROGRESS
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58842: gap of unknown length
91011: contig of 32169 bp in length
91211: gap of unknown length
104992: contig of 13781 bp in length.
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2.6%; Score 136.2; DB 68; Length
Best Local Similarity 43.6%; Pred. No. 4.6e-08;
Matches 1048; Conservative 0; Mismatches 1338; Indels
                                                                                                                                                                                                             Eukaryota; Alveolata; Apicomplexa; Haemosporida;
1 (bases 1 to 104992)
Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurdi, Cand Davis, R.W.
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                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum 3D7 chromosome 12
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HTG; HTGS_PHASE1.
malaria parasite P. falciparum
Plasmodium falciparum
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                                                                      catatgcaaatgatctcaatattaacataaaagaagctacaactaaaaataaaatacact
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AC004157 163226 bp DNA HTG 29-JUN-2000

LICCUS PLASMODIUM falciparum chromosome 12 clone 3D7, *** SEQUENCING

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                                                                                                                                                                                                               Direct Submission
Submitted (19-FEB-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                       Rowley, D., Mao, J., Tamaki, T.,
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                                                                                                                                                                                                                                                                    On Jun 29, 2000 this sequence version replaced gi:7243830.

NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5541: contig of 5541 bp in length
5741: gap of unknown length
72759: contig of 67018 bp in length
72959: gap of unknown length
88038: contig of 15079 bp in length
88238: gap of unknown length
163226: contig of 74988 bp in length.
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0; Mismatches 1338; Indels
nic, high agrasite P. falciparum.
Plasmodium falciparum
Eukaryota: Alveolata: Apicomplexa: Haemosporida;
1 (bases 1 to 16326)
Hyman, R.W. Chug, E.L., Qin, F., Rowley, D., Mao, J.,
Kurdi, C.B., Corway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
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                                                                                                104703 TATATAATAATAATATTATTTTTTTTTTTTTTTTAATTAATTAATTAATAATAA 104644
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3319 gtatggagttgatgaagacacttttgc-aattgcaaaatctagtattaccaactctttta 3377
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AE001398 AE001362 AE001398.1 GI:3845197
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CFAKFHENVDHIDNEKILNILRLYVDNSILDIDINNKMLCNLNNNLINENIEXISKLL
NEYCTLIKKGKYDNDMTIXKLKEYIKATHHILDINKTKILESTOSIDYSTLLNSLNNK
FILNKIIDKNITLEYECLLKILLINKFNHOSILDISIKNIYNIYILNNUYINNY
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INNNYSELYCNIEFEGERRATENBRAVLIHNNDQPNYSNKEBIKDIIQKRIKEY
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GLKKGSLKSKTRKSTSGSKFKPLNKYFLSKIKIVTSLNKIPSPLKEQKNTEVNLPESL
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KKILYIANNLYWYENYGYVCEMLERVISSHKEONLESYNYNKHVEHKHEDKILCHISE
DDYIEMSNYTWYLFYDYLKHINSEEDOSNILRNNSTNDRFIDENEKKYKLNNTTIKH
NNYKLNYEKSNYSHSYNSNGNISNILKEDDENOSNILRNNSTNDRFIDENEKKYKLONNTTIKH
CKDVLVHYEINNSNGNISNILKEDDENOSNIKNHNNVEMDLIDNKNENKKIOEKGONEENCEN
CKDVLVHYININTEGELKHEKKKELFFOLVMYLCHITKFKRRYVSSSSEFHMDVFKIIK
DMNLKYLCLENYKIKNEECAFLYTIDIVLFKER"
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EILGKICOKIMSYIHEMNGNELIHFLIYFFRWNKNDKNLILEYNYYFDHMYLFN
                                                                                                                            Gardner, M.J., Tettelin, H., Carucci, D.J., Cummings, L.M., Aravind, L., Koonin, E.V., Shallom, S., Mason, T., Yu, K., Fujii, C., Pederson, J., Shon, K., Jing, J., Aston, C., Lai, Z., Schwartz, D.C., Pertea, M., Salzberg, S., Zhou, L., Sutton, G.G., Clayton, R., White, O., Smith, H.O., Fraser, C.M., Hoffman, S.L. et, al.
Chromosome 2 sequence of the human malaria parasite Plasmodium
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Submitted (02-NOV-1998) The Institute for Genomic Research, 9712
Medical Center Drive, Rockville, MD 20814, USA
Location/Qualifiers
1. 14867
malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 14667)
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4;282(5395):1827]]
2 (bases 1 to 14867)
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| 11241... 14606
| /gene="PFB495w"
| /note="predicted by GlimmerM"
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/db_xref-"GI:3845198"
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complement(1570. .2424)
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ОщΣ	Query Ma Best Loc Matches	. Match 2.5%; Score 133.2; DB 31; Length 14867; Local Similarity 43.1%; Pred. No. 1.8e-07; les 1515; Conservative 0; Mismatches 1948; Indels 53; Gaps 16;
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g	10791	
oy B	592	caaaataatttatctattcaacagattcttttcaattagagagtattcaaaaacactaca 651
ò	652	actactgcttgcaactttctatcactgatatataaaagtgaaataaattaaaa 705
g	10671	TCTI
8 8	706	aactttagttttaatagaagaattttattaaaagctttgaatcaaatttaattactgata 765
δ. A	766	taaaaatactattaaacattaacaatgcttaattaaagtattattatttacct 818
δ	81	878
g	10491	
OY Db	879	cacttgatattataaataatcatataaactcccaaataaactattgcaaggttatggta 938
Οy	93	a 998
g	10371	ATTA-AAATAAATAGAAGTTTTTTAATAAAAATGTTAATTTTTGTGAAATAT-ATATA 10314
Q Q	999	tcctttaacattaaagttacacatgaaaaattagataatggaatggaagtatacgtgatt 1058
ò	1059	ccaaatcatogogoaccagoagtoatgoacatggtattatacaaagtoggtggaactgat 1118
q	10253	AATTITITITITACCATIATATACACTAAAAGATITITATAAACTITITIGGGGGAA 10194
දු අ	1119	gatccagtaggatactctggattagcacattttttgaacacttaatgtttagtggaaca 1178
ŏ	1179	1238
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οy	1239	acatotoaattttgtactatatactacgaattaataccaaaacaatatttat-otottgo 1297
qq	10075	ACTATTTTTTTAAAAATTAAAAATGTTTAATTCTTATGTAAATTATTAATAATAATAA 10016
ò	1298	aatggatattgaatcagacagaatgcagaattttaaggttaccgacaaagcattaataag 1357
QQ	10015	TAATAATATTAAATTCATTTATCATTTTAGTTCTTTTGTCATAAAAGGGATATTATATA 9956
oy G	1358	agaacaaaaggtagtcttagaagaaagaaaatgagagttgaaagccaagcaaa 1411
3	0 0	7
S S	1412	aaacatactagaagaagaaggaaaatgcattttattacaatggatatggcagaccagt 14/1
ò	1472	ttagcaactacaacaaagaagttgctgaagcct 1
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δγ	1525	ttcataagctacattatagtcctaataatgctatattaattgtaactggagatgcagatc 1584

gaatttcagcagaatatttagaaagtgcaaagtataaagta--aaagcacatttaactta 2062 taactccgctatggaaaatatctttcaaaacaatataagattaaccgggcatttattacc 2242 aagaaagcaggatacgcttatgatgcctttgataagcaaggacttgcatactttacatca 2482 aaaatattaaacgaaggatcaaaaaaacaactatgctctcagttttgcacaacaattagaa 2542 2603 acctta----tcagaaaactttgaagaagccctagttttactcagtgattgcatattcaa 2658 cacaagaagtaatcacacttgcaaaacaatactatgggaaaataccatctaataataaga 1644 aaccttcaagtcaagttagggtagaaccaccgcataaaacaaatatgactttaacattaa 1704 aagacagttcagtagaaatcccagaactgtttttaatgtatcaaataccaaatggtatta 1764 geetgetttacaatgatttggtaattaacaatecaatagttacategataaaaacagatt 1884 ataattacttaactgacagcgataattacctttccattgaagctatacctaaaaacggga 1944 1945 tetetacagaagetgtagaacaagaaatteataaatgtataaattatttagaaaatg 2004 2303 ttcaatacatatgcaaatgatctcaatattaacataaaagaagctacaactaaaaataaa 2362 atacactatctatatgttgaacatcataacctaccaacaatttccttaaaaatttgcattc 2422 AAATAAAATAAAATAAATTAATTAATTAAATTAAATTAAATTAAATTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAA AAAATTATATTAAAAAATTCATATATCATTATTTCAATTCAAAGTTGCTAAATTTTA 9601 9600 TATATTATTATAATAATATTATATTATTAATATAAATTAAATTGTATTAAATAAA 9541 ccaataaaaactacatacttaacatgatgttagcagaaatactcggtagtggtaaattca 1824 GACATAAAATATT-----ATGTAAAATATTACACGAATATATATATCATTTGTAAAATTAT ggcaaaggtatagacttaaaatttgatatagacctagacaatttttatatatcattaaaa 9715 1645 0996 1705 1765 1825 1885 9420 2005 9300 9180 9120 2243 0906 0006 8881 2483 8821 2543 2123 2183 2363 2423 ōλ QQ g QQ δy g Qγ O.Y Qy Oy οp οy Dβ ΟY ÓΫ Db Oy Db Qy Db qq οy qq οy g δλ Db δý Dp οy δλ

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                                         8641 TITAAAAATAATAATAATATTAATTAATGAATTAAAGCAATATTATTATAAA
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The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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aa, possible signal sequence, revised: added new exon 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 86827)
Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T., Churcher, C.M., Craig, A., Davies, R.M. Devlin, K., Feltwell, T., Gentles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S., Hornocks, P., Jagels, K., Jassal, B., Kyes, S., McLean, J., Moule, S., Mungall, K., Murphy, L., Oliver, K., Quall, M.A., Rutter, S., Skelton, J., Squares, R., Squares, S., Sulston, J.E., Whitehead, S., Woodward, J.R., Newbold, C. and Barrell, B.G.
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On May 5, 2000 this sequence version replaced gi:4493931.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
                                      ATATAATTAATTATTAAATAT-TAATTTTTGTTTTATATTAAATATATTATTATTATTAT 7383
                                                                                                                                                                                                                                                                                     PFMAL3P5 86827 bp DNA INV 04-MAY-2000 Plasmodium falciparum MAL3P5, complete sequence.
AL034556 AL008971 AL008972 AL008978 AL010141 AL010153 AL010162 AL034556.3 G1:7711064
HTG: centromere: CTRP protein; initiation factor E4; Scrinc/threonine protein phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The complete nucleotide sequence of chromosome 3 of Plasmodium
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                                                                                 gtaatcacaatatcaaattttctttacaggattatattgtgacctaccataacaacttat
                                                                                                                     ttattataagcttttaacctgggataatatgaagttttgctaatgttaagcaaaaaatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 86827)
Bowman,S., Skelton,J., Churcher,C., Lawson,D., Quail,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(322. .603,826. .1023,1197. .1301,1458. /gene="PFC0575w, MAL3P5.1"
join(603,826. .1023,1197. .1301,1458. .70ene="PFC0575w, MAL3P5.1" /note="PFC0575w (MAL3P5.1" /note="PFC0575w (MAL3P5.1). Hypothetical pro
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/strain="3D7"
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                                                                                                                                                                                                                                                                                                                                                       Nature 400 (6744), 532-538 (1999)
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/translation="MKKKKKHYFSIKFVNVDKNKYVLCSKDYIRIINYMIGLHIFRLL
QKIFHIYFANBQIASSFPESHKNYRVTKEDIIDGIEKCWFNITDYLISESIKQDNDFS
                                                                                                                                                                                   LKVKDEEIVSKKNNFSFSALSNDSNSVTKKYIVDLTLLDNIIESETKYNFASVGKVVV
TLKKEKKKIWNRLLLSKEKYPNMQVWWDMKEKRIHIITFVTINLFFLLSLSHRYHDSV
QNFLKEEKNNSDKLQDDIDEDEEKYFDEEILREAKKKSEEYDKDDEEL"
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                                                                                                                         NDIKTTVTAMKNKMDQLLTTSYSNKKIDTVNASFQWAQSPEYIFLNIKFSHRWSSPGA
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10613. .10674,10773. .10798,10929. .10999,11157. .11237,
11453. .11515,11715. .11767,11950. .12040))
/gene="PFC0582c"
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/note="potential splice accetor sequence for exon 11 of
                                                                                                                                                                                                                                                                                                                                                                       7790. .7799
/note="potential splice acceptor sequence for exon 2 of
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/note="potential splice acceptor sequence for exon 3 of
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/note="Potential splice acceptor sequence for exon 6 of
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/note="potential splice acceptor sequence for exon 7 of
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/note="potential splice acceptor sequence for exon 10
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/note="potential splice donor sequence for exon 10 of
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/note="potential splice acceptor sequence for exon 8
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/note="potential splice donor sequence for exon 6 .
PFC0581w"
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/note="potential splice donor sequence for exon 2
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/note="potential splice donor sequence for exon 3
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/note="potential splice donor sequence for exon 5
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/note="potential splice donor sequence for exon 7
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/note="potential splice donor sequence for exon 9
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/note="potential splice donor sequence for exon 4
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YSYDTMVNSFTFSYFFFSLSYLLFILFYHPDMYASYIFFKTLTYSGLPTYYYSLXNNI
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YPIIKNEKTVLDLLNYGYKIVMSPDVDNSLFEKTKIDSIPNEKDKNNQMENQKNSKNY
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/note="predicted splice donor sequence for exon 1 of PFC0575w (revised)"
PFG0575w (revised)"
Note="predicted splice acceptor sequence for exon 2 (revised of PFC0575w)"
1024...1039
/note="predicted splice donor sequence for exon 2 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFC0575w (revised) "
complement(3354. 6644)

Complement(3354. 6644)

/gene="PFC0580c, MAL3P5.2"

/note="PFC0580c, MAL3P5.2"

/note="PFC0580c (MAL3P5.2), Hypothetical protein, 1 1097 aa, possible signal sequence, predicted using hexexon"
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Protein_ad="Changag69.2"
/db_xref="GI:7711065"
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/product="hypothetical protein, PFC0581w"
/protein_id="CAB90285.1"
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Protein_de="CA88968.1"
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                                                                                                                                                                          tttacaatgatttggtaattaacaatccaatagttacatcgataaaaaacagattataatt 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atcagaaaactttgaagaagccctagttttactcagtgattgcatattcaacaccgtcac 2667
                                                                                                                                                                                                                                                                                                                                                                                      agcaggatacgcttatgatgcctttgataagcaaggacttgcatactttacatcaaaaat
                                                                                                                                                                                                                                              1891 acttaactgacagcgataattacctttccattgaagctatacctaaaaaacgggatctcta
                                                                                                                                                                                                                                                                               41405 TATATTTGTATAATAATAATATATATTAACTTAATATAAACAATATAAACAATATAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          acggac-taactttcatatcatatttttatggcatgcatctaatactaggagtaccgcta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATAATATAAATATATAAAATACAATTAAAATAAAATAAATTTCATAAAATAAATA
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                                  PFC0582c'
                                                                                                                                       Indels
                                                                                                 Score 128.4; DB 33;
Pred. No. 4e-07;
0; Mismatches 1196;
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revised: new gene prediction'
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Best Local Similarity 44.6%;
Matches 987; Conservative
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/note="PFC0575w, MAL3P5.1), Hypothetical protein, len: 689
aa, possible signal sequence, revised: added new exon 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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VHSILNGQISEKVYEKKOAENVIALHLFLLKDENITLFSMMHIMDFFKSKQKVIECIRD
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

L (bases 1 to 8087)

Bowman,S., Lawson,D., Basham,D., Brown,D., Chillingworth,T.,

Churcher,C.M., Craig,A., Davies,R.M., Devlin,K., Feltwell,T.,

Churcher,S., Gwilliam,R., Hamlin,N., Harris,D., Holroyd,S.,

Hornsby,T., Horrocks,P., Jagels,K., Jassal,B., Kyes,S.,

Moule,S., Mungall,K., Murphy,L., Oliver,K., Quail,M.A.,

Sulston,J.B., Whitehead,S., Skelton,J., Squares,R., Squares,S.,

Barrell,B.G.
                          On May 5, 2000 this sequence version replaced gi:4493931.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
Plasmodium falciparum MAL3P5, complete sequence.
AL03456 AL008971 AL008972 AL008978 AL010141 AL010153 AL010162
AL010206 AL010210 AL1199179
AL034556.3 GI:7711064
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Bowman,S. Skelton,J., Churcher,C., Lawson,D., Quail,M. and
Barrell,S.
                                                                                             gtatttttacttaattatttaattttatttttaaaataaaattacaattttacttactc
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/db_xref="GI:7711065"
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/organism="Plasmodium falciparum"
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3 (bases 1 to 86827)
Lawson, D., Bowman,S. and Barrell,B.
Direct Submission
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Nature 400 (6744), 532-538 (1999)
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On May 5, 200
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LOCUS
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join(7669. .7717,7800. .7829,7912. .7940,8064. .8106,
8302. .8368,8568. .8641,8713. .8812,8924. .9006,9122. .9258,
9369. .9505,9613. .9838)
/gene="PFCO581w"
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DINCERICLINYTYNIYITAFWYNIKIKTOKYNDHILLLLAWIHEDMKKKININTS
DINCERICLINYTYNIYITAFWYNIKIKTOKYNDHILLLLAWIHEDMKKKINOKONINTS
DINCERICLINGKNINTOKOUDDOWNHLHKKENDKFYNYSDHWHNIYKYISDNY
PYDHINSSARCSFKNLKKOQTDDNTKHIIMGKEKYPMNKSDHEKKNNNTGGNINIEK
POKKDILKYTYTYTEKGNKLDDOQINELELYWIYTMKLEPEGSKEKLISIKKHIHLLEKKANE
POKDNIIIYNNYDKETNKTTANNNNDNNDNICSNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICSNNNDHICKNKRKRY
YELAKIYTUNIFDYLKGKKRKHQNEDNTINLYYIKKKPWIFYLKNIIKNCOTSFIEH
NNNIVONDIKNNNIIERKKYNLFESSIISYPYIKKHPWIFYLKNIIKNKFÇK
                                                                                                                                                            DIYNDDDDYDYEKEEDLVIQKNIDDYIYKNTIGMNKSLEEFKNQFIEGADIEFQNFLS
WUDDQHEKYKSUDENTKESTEHIKKKNTINKCYDTELIQNOKENNFIKRIKNIDNISND
ISNNEINIIKLKKLNQSDEDINLTSDLIZERLKYVLWYIQKIEYLKEKYQYDIINEQ
YPIIKNEKYYLDLLAKYGYKIYMSPDVONSLEEKTKIISIPNEKDKNNOMENQKNSKNY
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/translation="MLGLKRKNVFYLLVSVPSLFAVFLKRHKDNENNYETLINNNDIE
KRIKIRIHNENCSYIPLEFLNIYDSYIPKNKILINHLYFFRRKREBEYYYITHWYRK
KRREAIKYNFISDEONIENNEYYIETVLEVSEKYGILSPHLSELYINISHOVNIYP
SLYYYNKLDNKHNLINEKKLKYFKQINNEHTQQAPINHTHHNNNNNKKPLDINIHSC
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LKKKDEELYSKKNNFSFSALSNDSNSYTKKITVDLTLLDNITESETKYNFASVGKVVV
TLKKEKKKIWNKLLLSKEKYPWOVWWDMKBKIHIITEYTINLFFLLSLSHRYHDSV
ONFLKEEKNNSDKLODDIDDDBEKYFDEEILREAKKKSEEYDKDDEEL
IKSKKKRKRULSIYINLFICTLIYFTYCMCLLIKYISHLCIFFFFCFFLCYNILER
IEECVGOLIKKEIRYNLYCEKKKIKFHMKDAIKKMEINMODDLYFRYYDDELLRC
FYMKLNIERNKNIISHNYONINNDISIOPOMYMNPIDVNINNISLOEKIKOOFEND
DOBNIKELKOIYSOFOLFNDNIIKYIEEDQPLYNINDNSNINDNNINTMKHKIK
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IDIVKFKDLYYCMINNINNIFSYIHKVDHNECVYRIFKAYNKILLYEYNYLNEKENIY
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LYTORIONCCDIFSYIYKKYNFNEKNPFLNYLYYELHYIYYSEKKKKKFFSFISSSP
XSYDTMYNSFIFSYFFFSLSYLLFILFYHPDMYASYIFFKTLTYSGLPTYYYSLYNI
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QKIFHIYFANEQIASSFFESHKNYRVTKEDIIDGIEKCWFNITDYLISESIKQDNDFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="PFC0580c (MAL3P5.2), Hypothetical protein, len:
1097 as, possible signal sequence, predicted using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          jóin(7669. 7711,7800. .7829,7912. .7940,8064. .8106,
1930. .8368,8568. .8641,8713. .8812,8924. .9006,9122.
19369. .9505,9613. .9838)
/gene="PECÓ581w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="predicted splice acceptor sequence for exon 2 (revised of PFC0575w)"
1024. 1029.
1024. 1029.
Foredicted splice donor sequence for exon 2 of PFC0575w (revised)"
complement(3354. .6644)
complement(3354. .6644)
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                                                                                                                                                                                                                                                                                                                                                                   604. .609
/note="predicted splice donor sequence for exon 1
PFC0575w (revised)"
816. .825
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/product=hypothetical protein, PFC058lw"
/protein_id="CAB90285.1"
/db_xref="G1:7711066"
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/product="Hypothetical protein, PFC0580c"
/protein.id="CAB38968.1"
/db_xref="G1:4493932"
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complement(join(10024. .10044,10320. .10336,10397. .10445,
10613. .10674,10773. .10798,10929. .10999,11157. .11237,
11453. .11515. .11767,11950. .12040))
/gene="PFCO582c"
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10613. .10674,10773. .10798,10929. .10999,11157. .11237,
11453. .11515,11715. .11767,11950. .12040))
/gene="PFCO582c"
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/note="potential splice accetor sequence for exon 11 of
PFC0581w"
                                                                                                                                                                              of
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/note="potential splice acceptor sequence for exon 7 of
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/note="potential splice acceptor sequence for exon 9 of
                                                                                                                                                                                                                                                                                                                                                                                           note="potential splice acceptor sequence for exon 4 of
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Anote-"potential splice donor sequence for exon 10 of
PPC0581w"
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                                                                                                                                                                                                                                            7941. 7947
/note="potential splice donor sequence for exon 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8642. .8647
/note="potential splice donor sequence for exon 6
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Anote-"potential splice donor sequence for exon 7
PPC0581w"
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/note="potential splice donor sequence for exon 5
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PFCO581w"
7830. .7835
/note="potential splice donor sequence for exon
                                                                                                         PFC0581w"
7001. 7911
/note="ptential splice acceptor sequence
PFC0581w"
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/protein_id="CAB90286.1"
/db_xref="G1:7711067"
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18;

59; Gaps

Indels

Length 86827;

DB 33;

Score 124.2; DB 33; Pred. No. 1.2e-06; 0; Mismatches 2258;

Query Match 2.3%; Best Local Similarity 42.6%; Matches 1718; Conservative

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AAATITITITATTATAAATGAGGATACGAAGGTTATAATGTTTAATATGAGATATATAGA 37980
                               37086 TAATAAAATTTGACAAAAAAAAAAAAAAAAAAAAATAGAATTATTTTCCCTTTAATTTCCTG 37145
                                                                                                37506 TCTTTTATTTATATTATATGAATGCTCATTTTTATATGTACTATTTATATTTATAT 37565
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                                                                                                                                                                                                                                                                                                    37326 TITITTATITTATGATTTAACCCGTTCATTCTTTTATCTTATTAGAACAAAGAAAT
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                                                                                                                                                                                                                                                                              243 gtatctcatgtatttgtaaaaccaggagaacaaaattgattttctaccgcgcagaaaat
                                                                                                                                                                                                                                                                                                                                                                                                                   agtaggaaaatattttaataaggtagcttgtt--tttgtttcaccaaacaaacattatac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37686 TTGGATTTTTCCAAATAAAAATAACAAAATATTCAAAATGAATATAATATTTCATAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   774 ctattaaacattaacaatgcttaattaaagtattattattaccttaatttcataacctt
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                                                              tctatgatatgtttagtgtacgcttctgtaccactatatagtatattttgtaaagtaaca
                                                                                                                                        ggttatggaggtacagtaagaacaagtaatatatcaaattctaaaataggtaacactatt
                                                                                                                                                                                                          attaaagtcagatttaatgcagatatacacaaacaactgccatggaaattctatccagaa
                                                                                                                                                                                                                                         37266 ATABATCITTABAATGAATCATABAATATAAATAAATATATACAATAGTGTATTTCAATA
                                                                                                                                                                                                                                                                                                                                                 303 cta-----cttgatgaggacacttcaggaatggctgtatataatgttacaccacataa
                                                                                                                                                                                                                                                                                                                                                                                  37386 ATATGATTATGTTAATAAATAAAAAAAAAGGTATGAAACTCTTTAAGAAATGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cctcatcaaaaaactataatgccagtatcattttttatagatccagccatagaaacagat
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tcaaataaaatgaaaccaagaataagaaacactatttatggattaatagcaataatacta
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39777 ATATTAATAATAAATAAATTATTTTTTTTTTTTCCACTTAATATATATATTAAAATA 39836 ttaatgatagaattaa---gagacaagttaggattaacataccatagtagcagttcacta 3211 tctaacatgaatcatagtaatgtgctatttggtacaatattcactgataataccacagta 3271 aacaactatgeteteagttttgcacaacaattagaaggcaaaggtatagaettaaaattt 2566 ctttgataagcaaggacttgcatactttacatcaaaaatattaaacgaaggatcaaa--a 2747 gctacaacagaaatgaatcacgctatattcaaagggcacccatattctaacaaagtttac agttttgacaaggaacaaatcgttatcagcgcagcaggagatgtagatccaacacagcta 2927 tcaaatttactagataaatatattctttccaaattgccatctggtaataacaaaaatacc caaagtgtcataatgtttgctacagacacagtaccatatcacagcaaaga-----gatatagacctagacaatttttatatatcattaaaaaccttatcagaaaactttgaagaa gocotagittitacicagigatigoataticaacacogicacagatcaagaaataticaat 39956 AATITAAATTAAAATAAATTAAATGTTTACTTATAAATAAAT----TAATTAATTCATTT ataccagatacgactgttaatagagaagacacattattatatgtacagagagatgtacca taacctaccaacaatttccttaaaatttgcattcaagaaagcaggatacgcttatgatgc agaataatagcagaacagattgcacatgttaaatcattatattctgctcctgaatttata aaaacaatataagattaaccgggcatttattacctaatggagaatagttatgagaaacat 2269 attgtgtttacacattaatattgattttcttttcattcaatacatatgcaaatgatctcaa 3212 2987 2687 3047 40193 2209 2389 2627 g Ωÿ 07 07 07 ga A g Qy Db 9. 0.0. Qy Db οy QQ οy ò Qy Db g Dp δλ 8 Οy qq QY Db δy 셤 δ δy g Ω

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TEARLY TOTAL TOTAL TO THE TRAINGLEY TEST PELKSNELK INDLRY ISTUNKYKY
LOIKKRSNLKKNHNIRKMEDNESSFIDIGSNLTDKMFDGVINSKKHENDLONVLNRAK
NNNVDKITITCTCLAEIDKGLKICFTYDPEGKFLYLEAGVHPTNCYFEIDKKHKEBKE
ITAKKFYEFEFTKYFKNEGVENSKMENGNKTCDGFKDMINLNEILLEKNLDTIPGFKY
NERDKEYLENLKKHIKYPRRIVCTGEIGLDFDRLYFCSKYIQIKKFIFOLKUNGKY
LPMFLHMRNCSETFFKIVDIYKFLFEKNGGVIHSFTDKEDIVHIIVONYKNLYIGVNG
CSLKSLENINAVKKIPLNLLLLETDAPWGGVKKTHASYEXIKDTYEKRAKIKN
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GDIOELPHTCRNFDVPYYASKLEENLRDIEVEDSEFYSEKNSNEHVLHHCNSNDASE
KKYNVYYHNILWSILKTFKRIILIISTYILETLUVTLGGKFIDYYMRILEGOKIPV
YISFLKDFKVFSGIVVWMIMFFHLFFEALLHFYFHLFTINLKVSLWYFLYKINLCSNN
NHLQNPDAFYNTYRKFSSQTEIDEISRDFLSIGKNASSSSSGIKNNNKNIDNNKFVEN
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AMRKLLSGEINSIKLDNGDELKIKLNDEKHKDSTKWDKSYSFISNLEEEKYSGTDLFR
KKQEINEANTKIIEDRQEFYILNNDEIENIATRFVLENNFDELYIQSFKQSLIDIIQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"conserved hypothetical protein, UPF0006 family"
/protein_id="CAB63556.1"
/db_xref="GI:6594244"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8020. .10389
//note="possible cent, region of very high [A+T] content"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MALIP3.01, conserved hypothetical protein, len: aa, similarity: UPF0006 family eg to YBL0552C/YBL0512/YBL0511, YBF5_YEAST (418 aa), fasta scores: opt: 316, E(): 1.1e-12, (33.2% identity in 271 overlap)"
more information about this sequence or the Malaria Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MAL1P3.03, putative ABC transporter, len: 1822
                                                                                                                                                                                                                                                                                                                                                                                                                  .2598,2748. .2848,2990. .3276))
                           see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be
                                                                                                                                                sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2599. .2610)

/note="potential splice acceptor sequence"

complement(2742. .2747)

/note="potential splice donor sequence, atg/gttaaa"

complement(2849. .2861)

/note="potential splice acceptor sequence"

complement(2849. .2899)

/note="potential splice donor sequence, aaa/gtaaaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5005. .5496
/gene="MALIP3.02"
/note="MALIP3.02, hypothetical protein, len: 163
contains possible signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2848,2990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein, MAL1P3.02"
/protein_id="CAB63557.1"
/db_xref="GI:6594245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative ABC transporter"
/protein_id="CAB63558.1"
/db_xref="G1:6594246"
                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(1748. .2598,2748. /gene="MALIP3.01" complement(join(1748. .2598,2748. /gene="MALIP3.01"
                                                                                                                                                                                                                                                                                             /organism="Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:5833"
/chromosome="1"
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14884. 203=
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5005. .5494
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                                                                                                                                                                                                                                                                                                                            /strain="3D7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 67970)
Bowman, S., Churcher, C., Harris, B., Harris, D., Lawson, D., Quail, M. and Barrell, B.
41029 ATTATTATTATTATGTATTTAATTATTTATGAAATTTATTTAATTAATTATATTTATATAT 41088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10493 TITIATITIAATITAATITIAATITIAATITA--TITATATITAAAGTATITAATIT
                                                                                                                                                                                                                                                                                                                                                                                                                     gagttatattaataaatacaattcttactacaaagcaataacaatagaagaagtaaataa
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                                                                                                                                                                                                                                                                                                   gttaaataacaataatgttagtgagatattgttaagcttacaattacacgatctagatcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cataaatggcaaacaaatagatgctaaaaaacacataccttggttaagtatacaggttat
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On Dec 16, 1999 this sequence version replaced gi:5763807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFMAL1P3 67970 bp DNA INV
Plasmodium falciparum MAL1P3, complete sequence.
AL031746.9 GI:6594243
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Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3981 aaaagcagttatact 3995
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RESULT 13

PFMAL1P3

3921

3801

DEFINITION

ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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RFKRIIAEASEEQKYPWEEDFCLILNEEELIRPEHNDSPYLPEHYENIDKINELSINS
TKIWKETIKKMRQNYEKETDNMNHNWRDFWHYKWANIYLYKVHKLINITLKDLTNPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /_octe="MALIP3.04, conserved hypothetical membrane protein, len: 203 aa, similarity: P. falciparum chromosome 2, PED110W, 096126 predicted integral membrane protein (255 aa), fasta scores: opt: 335, E(): 4.9e-15, (36.1% identity in 191 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MRIKMNSGIFFIKLLICISFICVFECFNKCMISYRKDLLWYSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CENY SIDRSLAEGSSESKETKVKDIPNIELLKSLNINY EEYEKMKEIVGSFMDNNNLN
IANEVLKNIHSFTNIENIFSLINDSSKSPVLKTFLKEFGSIFPHMLNNVPKLLFDLCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSTLGYCISFSARLGVIIKFLLCDYTHIEKEWCVQRLEEFAKISNKENASMNKENEL
NVITTQTYKERNENISDKISAIVEYKNVSLSSIINSSQDDESKKYGIKFENVYVSYK
KKIPLVNGTYKYIDEEPSLKNINMYALKNQKIGIVGKSGAGKSTILLSILGLINISQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIIVEGRDIRTYNRKGEDSIIGILAOSSFVFYNWNIRTFIDPYNNFTDDEIVHALKLN
GINGKNDLYKYMHKODMKSNYKKIIOTSKVINOSNDNTILLTNDCIRYLSLVRLYLN
RHKYKIILIDEIPIFNLNNSVHDELNSFLIGKAKSFNYIIRNHFPNNTVLIISHHANT
                                                                                                                        MFKYFFYHKMYHKNIINKQILSGLLKNVDDNTNKKICFQEHKSNSTYNYNSSHIHE
KKEEYENIHNSSNSTMSNEFKEKKKNNEYIIKLENCSFGLSYDNKCDNDHILKNINFN
                               YLKDRLNKKEEIKFTSIIMPLYVYKILLSNVANFPNLVNNVMEGIVNIKRLNNYINDH
LYYNDIKNYEMYRTRYNEDYNIVVDKTFLQNENITSHDDGTSHNLKHLKNVIKNKLTN
                                                                                                                                                                                                                 LKRNSLAIIIGNVGSGKSAFFHSILGDFNATHGNLYIENFFKKMPILYVPQNSWLFMG
NIRSMILFGNEYNPLIYKYTILQSELLNDLSTIEHGDMKYINDDHNLSKGQKVRICLA
KEFKLIKMFNWESFAFKYINIFRMKEMKYCKIRLYLSNIGVFISSISSDIVEVVIFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="region containing small subunit, 5.8S and large subunit rRNA genes and spacer regions" . 31533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(32477. 32486)
/note="potential splice acceptor sequence"
complement(32669. 32674)
/note="potential splice donor sequence, aaa/gtatat"
join(36657. 36743,36864. 37343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="potential splice donor sequence, aag/gtatga" 36854. .36863
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MAL1P3.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MAL1P3.05, hypothetical protein, len: 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"potential splice acceptor sequence" complement(join(38049. 39995,40210. 40284))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(31966. .32476,32675. .32775))
/gene="MALLP3.04"
complement(join(31966. .32476,32675. .32775))
/gene="MALLP3.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HDKEETITTWIKWIQEDIEYFLFNLQVEWLRILTLELFYKNKE"
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/protein_id="CAB63560.1"
/db_xref="GI:6594248"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSCCDYIYVLRKGEITYRCSYEDVKTQSELSHLLEMDD"
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RNPLHIILGLIVILAAIYVFENFKNFEC"
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/db_xref="GI:6594247"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23896. .31533
/gene="rRNA"
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/translation-"MEQIGTANNIFTEIGKNIVKRSGPFEIWRKFIEEVSKKISNSL
NIENIKECKKNCRKINYWMDDKEEEFVSKKFFVYEYIISNVWKNEFEKAIINTLKNKT
KTCLRSRKKYPKEIRNIMGELEDYIDAINDYKKOFKNLYCWSERYIDYKKWLNEMKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                  /note="WALLF9.06, garp, len: 673 aa, similarity: almost identical to GARP_PLAFF (678 aa), fasta scores: 97.6% identity in 678 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aa.
                                                                                                                                                                                                                                                                                                                                                                   DDDAEEDDDDAEEDDDEDEEDEEEEEEEEKKIKRNLRKNAKI
complement(39996. .40005)
/note="potential splice acceptor sequence"
complement(40204. .40209)
/note="potential splice donor sequence, aag/gtaaca"
join(45401. .46396,46562. .50233)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              610 caacagattetttteaattagagagtatteaaaaacaetacaactactgettgeaaett
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/gene="MALIP3.07"
/note="MALIP3.07, hypothetical protein, len: 1555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 33; Length 67970;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="hypothetical protein, MALIP3.07"
/protein_id="CAB63562.1"
/db_xref="G1:6594250"
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.39995,40210.
                                                                                                          /product="hypothetical garp protein"
/protein_id="CAB63561.1"
/db_xref="G1:6594249"
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Pred. No. 1.5e-06;
0; Mismatches 1187;
complement (join (38049.
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ilarity 43.5%;
Conservative
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Best Local Similarity
Matches 935; Conserv
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                                                                                                                                                                                                                                                                                  tgagagttgaaagccaagcaaaaacatactagaagaagaagatggaaatgcattttatt 1449
tttttgaacacttaatgtttagtggaacagaaaatttcctaatctcatcagcacactta 1209
                                                                                                                                                                                     acaatggatatggcagaccagtagtaggatgggaacatgaaattagcaactacaacaaag 1509
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                                                                                                                                                                                                        ATACGCTAATAAATAAATATATAAAAATATAAAAATAAAATAAAATTAAATTAAATTAAATTA
                  ttttcttaacaatagccaatcatgctttatcctttaacattaaagttacacatgaaaat
                                   tagataatggaatggaagtatacgtgattccaaatcatcgcgcaccagcagtcatgcaca
                                                                       8361 ATATTAAATAAATTAAATAAATATTAAAATATATATAAATTAAATAATAATAATA
                                                                                                                                                1690 tgactttaacattaaaagacagttcagtagaaatcccagaactgtttttaatgtatcaaa
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                                                     1030
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1 (bases 1 to 4601)

Lewis, D.L., Farr, C.L., Farquhar, A.L. and Kaguni, L.S. Sequence, Organization and Evolution of the A+T Region of Drosophila melanogaster Mitochondrial DNA

Mol. Biol. Evol. 11, 523-538 (1994)
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Blochemistry, Michigan State University, East Lansing, 1
48824-1318, USA
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                                              caattcaattaatgatagaattaagagacaagttaggattaacataccatagtagcag
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Drosophila melanogaster. Mitochondrion Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

/product="tRNA-Ile"

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ALIGDOINNIVTARAFIMFEWWRPIMIGFGGWMYDFLAMGABONGTSLSILIRAELGHPG
ALIGDOOINNIVTARAFIMFEWWRPIMIGFGGWMINPLAMGAPDWAFPRNNNMSFW
LLPPALSLLLUSSWVENGAGTGWTVPPPLSAGIAHGGASVDLAIFSLHLAGISILGA
VNFITTYINNRSTGISLDRWFLFWWSVVITALLLLSLPVLAGAIFWLTDRALTS
FDPAGGGDPILYQHLFWFFGHPEVYILLLFGFGMISHIISOESGKKETFGSLGMIYAM
LAIGLLGFTWAHHMFTVGMDVDTRXFTSAFMIIAVPTGTKTFSWALTHGTYDLSYS
PAILMALGFVELFTVGGLTGVVLANSSVDILHDTYVVAHFHYVLSMGAYPAIMAGF
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IVSTIGSTISLLGILFFFFIIWESLVSQNQVIYPIQLNSSTEWYQNTPPAEHSYSEEP
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3083. .3767
Anote="Taxa stop codon is completed by the addition of 3' A
residues to the mRNA"
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lefnnynnrellhgoliemiwtilpaiillftalpserllylldeinepsytiksigh
owywsyeysdfnniefdsymiptnelmtdgfrlldydnryvlpwnsoirilytaadyi
hswtypalgykydgtpgrlnotnffinrpgleygocseicganhsfmpiviesypvny
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NLNSMNWKW"
                                                                                                                                                                                                                                       /translation="mrnnsskilfitimiigTlitutsnswlgammgleinllsfipl
LSDNNNLMSTEASLKYFLTQVLASTVLLFSSILLMLKNNMNNEINESFTSMIMSALL
LKSGAAPFHFWFPNMMEGLTWMNALMLMTWQKIAPLMLISYLNIKYLLLISVILSVII
                                                                                                                                                                                                                                                                                                         GAIGGLNOTSLRKLMAFSSINHLGWMLSSLMISESIWLILFFFYSFLSFYLTFWFNIF
KLFHLNQLFSWFVNSKILKFTLFMNFLSLGGLPPFLGFLPFWLVIQQLTLCNQYFWLT
IMMMSTLITLFFYLRICYSAFMMNYFENNWIMKMNMNSINYNNYMIMTFFSIFGLFLI
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/protein_id="AAC47813.1"
/db_xref="GI:1166532"
                                                                                                                                                                   /product="NADH dehydrogenase subunit 2"
/protein_id="AAC47811.1"
/db_xref="GI:1166530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"cytochrome c oxidase subunit
/protein_id="AAC47812.2"
/db_xref="G1:7412849"
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/transl_except=(pos:3767,aa:TERM)
/transl_table=5
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/product="tRNA-Tyr"
join(1470. .1472,1474. .3009)
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/db_xref="G1:1166533"
                                                                                                                                                                                                                                                                                                                                                                                                                         /product="tRNA-Trp"
complement(1322, 1383)
/product="tRNA-Cys"
/product="tRNA-Gln"
171. 220
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3840. .3906
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3907. .4068
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                                                                           ="tRNA-Phe"
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/codon_start=1
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                                                                                                                                                                                      2 (bases 5269 to 5695)
Clary,D.O., Wahleithner,J.A. and Wolstenholme,D.R.
Transfer RNA genes in Drosophila mitochondrial DNA: related 5'
flanking sequences and comparisons to mammalian mitochondrial tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 (bases 14215 to 14512)
Ballard,J.W., Olsen,G.J., Faith,D.P., Odgers,W.A., Rowell,D.M. and
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/organelle="mitochondrion"
/db_xref="taxon:7227"
/note="derived from new and previously submitted
sequences; sequence is a composite containing sequences
obtained from different Drosophila melanogaster strains"
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Evidence from 12s ribosomal RNA sequences that onychophorans are modified arthropods
Science 258 (5086), 1345-1348 (1992)
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Satta,Y. and Takahata,N.
Evolution of Drosophila mitochondrial DNA and the history of the
melanogaster subgroup
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Lewis,D.L., Farr,C.L. and Kaguni,L.S.
Drosophila melanogaster mitochondrial DNA: completion of the nucleotide sequence and evolutionary comparisons
Insect Mol. Biol. 4 (4), 263-278 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Satta,Y., Ishiwa,H. and Chigusa,S.I.
Analysis of nucleotide substitutions of mitochondrial DNAs
Drosophila melanogaster and its sibling species
MOI. Biol. Evol. 4 (6), 638-650 (1987)
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       Pterygota, Neoptera, Endopterygota; Diptera; Brachycera, Muscomorpha, Ephydroidea, Drosophilidae; Drosophila. 1 (bases 12511 to 12682) Clary, D.O., Goddard, J.M., Martin, S.C., Fauron, C.M. and
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Nucleic Acids Res. 10 (21), 6619-6637 (1982)
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Lewis,D.L., Farr,C.L. and Kaguni,L.S.
Direct Submission
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Genetics 118 (4), 649-663 (1988)
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Garesse, R.
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                                                                                                   Wolstenholme, D.R.
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                                                                                                                                                                                                                                                                                                                /product="NADH dehydrogenase subunit 3"
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GLYHEWNOGMLNWSN"
                        /translation="MMTNLFSVFDPLAIFNFSLNWLSTFLGELLMIPSIYWLMPSRYNI
WMSTLLTHERERTLLGSGHNGGTPFIFISEESLEILENNHWGLFPYITTSTSHLTLT
LSLALPLWLCFMLYGNINHTOHMFAHLVPQGTPAILMPFWVCIETISNIITSTSTHTLL
LTANMIAGHLLLTLGNTGSSMSYMLMTFLLMAQOIALLVLESAVAMIQSYVFAVLSTL
                                                                                                                                                                           /translation="MSTHSNHPFHLVDYSPWPLTGAIGAMTTVSGWYKWFHQYDISLF
VLGANITILIYVYGWRADVSREGTYGGLHTYAYTIGLRAGMILFILSEVLFFVSFWAF
FYSLSPAIELGASWPPWGIISFNPGYPLALLASGWILYTWAHHSLMENNHSOT
TOGGLFFTVLLGIYFBYIEAPFTIADSIYGSFFPMATGFHGIHVLIGTTFLLV
CLLRHLNNHFSKNHHFGFEAAAWYWHFVDVVWLFLYITIYWWGG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_except=(pos:complement(6401. .6402),aa:TERM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complement(6337. .6401)
/product="tRNA Phe"
complement(6401. .8124)
/once=="TAA stop codon is completed by the addition residue to the mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cactgatatataaaagtgaaataaatttaaaaaactttagttttaatagaagaattttat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ttataaactgattaaaaaaaaataactattaatattgagcaaaataatttatctattcaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    taaaagctttgaatcaaatttaattactgatataaaaaatactattaaacattaacaatgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                     'product="cytochrome c oxidase subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 123.6; DB 33;
Pred. No. 2.2e-06;
0; Mismatches 1914;
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/db_xref="G1:1166534"
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5608. .5961
                                                                                                                                                                                                                                                                                                                                                                                                                /product="tRNA-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                               5055. .6118
/product="tRNA-Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"tRNA-Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="tRNA-Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="tRNA-Glu"
                                                                                                         /codon_start*1
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                                                                                                                                                                                                                                                                                       start-1
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Best Local Similarity 43.6%;
Matches 1547; Conservative
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17719 17538 AAAATITATATTAAATITATTTAAATTTAATTT-------TTCTATATATAA 17491 1811 ataaaaacagattataattacttaactgacagcgataattacctttccattgaagctata 1931 17947 TATATAA-----ATATTCAATATATATAATTTATAATTTATAATATAATATAATT agagttgaaagccaagcaaaaaaaacatactagaagaagaaatggaaaatgcattttattac aataaactattgcaaggttatggtaatgatgaaatttttttacttgtttttcatagtttt gttgctgaagcctttcataagctacattatagtcctaataatgctatattaattgtaact 18067 ITAAAAAACATGATTTTATTATAAATATTTTTTTATAAAAATAATACATTTAAGAAATT tttgaacacttaatgttttagtggaacagaaaaatttcctaatctcatcagcacacttagt TITATAAATTATATCTACATTITTAAATTTTAAAATTTTTAAATTAAATTAGATATA actttaacattaaaagacagttcagtagaaatcccagaactgtttttaatgtatcaaata ccaaatggtattaccaataaaaactacatacttaacatgatgttagcagaaatactcggt cttaacaatagccaatcatgctttatcctttaacattaaagttacacatgaaaaattaga taatggaatgga--agtatacgtgattccaaatcatcgcgcaccagcagtcatgcacatg gtattatacaaagtcggtggaactgatgatccagtaggatactctggattagcacatttt aatataggcggaaatttcaatgcaagcacatctcaattttgtactatatactacgaatta aatggatatggcagaccagtagtaggatgggaacatgaaattagcaactacaacaaagaa ggagatgcagatccacaagaagtaatcacacttgcaaaacaatactatgggaaaatacca tctaataataagaaaccttcaagtcaagttagggtagaaccaccgcataaaacaaatatg agiggiaaattcagcctgctttacaatgatttggtaattaacaatccaatagttacatcg aaatactttactcttatttttttatcacttgatattattaaataatcatataaactccca

TTATATATATTTAATTGAAAATTAAATTATATGTATATATATATAAAATATGAATTGAAT 16232 17072 TITITITIATATATATATATATATATATAATTAATTATTTCAGATTTAGTGATTAAAATAA 16652 actatgeteteagttttgeacaa--caattagaaggeaaaggtatagaettaaaatttga 2568 tatagaccta----gacaatttttatatatcattaaaaaccttatcagaaaactttgaag 2624 acacagetatcaaatttactagataaatatattettteeaaattgeeatetggtaataae 2977 aaagtttacgggacattaaatacaatcaataatatcaaccaggaagacgttgcattatat gattaaccgggcatttattacctaatggagaatagttatgagaaacatattgtgttacac atagaataatagcagaacagattgcacatgttaaatcattatattctgctcctgaattta t-----agctacaacagaaatgaatcacgctatattcaaagggcacccatattctaac 2858 ataaaaaatagttttgacaaggaacaaatcgttatcagcgcagcaggagatgtagatcca 16951 AATTATATGTATATATATAAATATGAATTGAATTTTTATAAAAATCATTTTAAAT attaatattgattttcttttcattcaatacatatgcaaatgatctcaatattaacataaa 2391 acctaccaacaatttccttaaaatttgcattcaagaaagcaggatacgcttatgatgcct aagccctagttttactcagtgattgcatattcaacaccgtcacagatcaagaaatattca tatttagaaaatggaatttcagcagaata---tttagaaagtgcaaagtataaagtaaaa TITITITAAAAAAAATATITITITAAGTITITAATIATAATAATAATTATATAGGGG catgcatctaatactaggagtaccgctatcagaaatcagtaatatttacgataccatagacaaagtaagtatccaagatgttaactccgctatggaaaatatctttcaaaacaatataa 16831 ITAITATAAAAATAGITITAATAAGTATAATITAAAAAAATCATITITITTAAAAAAAAA ttgataagcaaggacttgcatactttacatcaaaaatattaaacgaaggatcaaaaaaca gcacatttaacttatgcatttgacggactaactttcatatcatattttat-----gg 2745 2798 2918 2049 2451 2625 16531 2685 16351 16291 1992 2102 2161 2511 16651 1932 17251 17191 17131 2221 2281 16711 g ö g ò 셤 g & q 요 Q Q ò g ò g δ g ò g 9. 9. ò g ò ò g ò g g Qy Dp δ δ ò ò

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15155 AAATTA 15150 caataa 3982

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